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Changes in salivary analytes in canine parvovirus: A high-resolution quantitative proteomic study.

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Abstract

The present study evaluated the changes in salivary proteome in parvoviral enteritis (PVE) in dogs through a high-throughput quantitative proteomic analysis. Saliva samples from healthy dogs and dogs with severe parvovirosis that survived or perished due to the disease were analysed and compared by Tandem Mass Tags (TMT) analysis. Proteomic analysis quantified 1516 peptides, and 287 (corresponding to 190 proteins) showed significantly different abundances between studied groups. Ten proteins were observed to change significantly between dogs that survived or perished due to PVE. Bioinformatics' analysis revealed that saliva reflects the involvement of different pathways in PVE such as catalytic activity and binding, and indicates antimicrobial humoral response as a pathway with a major role in the development of the disease. These results indicate that saliva proteins reflect physiopathological changes that occur in PVE and could be a potential source of biomarkers for this disease.

KEYWORDS: Bioinformatics; Biomarker; Canine parvovirosis; Dog; Label-based proteomics; Saliva

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